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RAW SEQUENCE LISTING

DATE: 03/26/2002

PATENT APPLICATION: US/10/062,375

TIME: 09:30:31

Input Set : N:\Crf3\RULE60\10062375.raw

Output Set: N:\CRF3\03262002\J062375.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Sutcliffe, Gregor J.
6 de Lecea, Luis
7 Siggins, George R.
8 Henriksen, Steven J.

10 (ii) TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,
11 COMPOSITIONS AND METHODS

13 (iii) NUMBER OF SEQUENCES: 26

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
17 (B) STREET: 10666 North Torrey Pines Road, TPC-8
18 (C) CITY: La Jolla
19 (D) STATE: California
20 (E) COUNTRY: US
21 (F) ZIP: 92037

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/10/062,375
C--> 31 (B) FILING DATE: 30-Jan-2002
32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US/08/857,389
36 (B) FILING DATE:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Schmonsees, William
41 (B) REGISTRATION NUMBER: 31,796
42 (C) REFERENCE/DOCKET NUMBER: 22908-0002

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: (415) 324-7041
46 (B) TELEFAX: (415) 324-0638

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 438 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: cDNA

59 (iii) HYPOTHETICAL: NO

ENTERED

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61 (iv) ANTI-SENSE: NO

63 (ix) FEATURE:

64 (A) NAME/KEY: CDS

65 (B) LOCATION: 30..368

68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

70	AAAGCACAGA CTTCAGGTTT CCAAGGAGG ATG GGT GGC TGC AGC ACA AGA GGC	53
71	Met Gly Gly Cys Ser Thr Arg Gly	
72	1 5	
74	AAG CGG CCG TCA GCC CTC AGT CTG CTG CTG CTG CTG CTC TCG GGG	101
75	Lys Arg Pro Ser Ala Leu Ser Leu Leu Leu Leu Leu Ser Gly	
76	10 15 20	
78	ATC GCA GCC TCT GCC CTC CCC CTG GAG AGC GGT CCC ACC GGC CAG GAC	149
79	Ile Ala Ala Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp	
80	25 30 35 40	
82	AGT GTG CAG GAT GCC ACA GGC GGG AGG AGG ACC GGC CTT CTG ACT TTC	197
83	Ser Val Gln Asp Ala Thr Gly Gly Arg Arg Thr Gly Leu Leu Thr Phe	
84	45 50 55	
86	CTT GCC TGG TGG CAT GAG TGG GCT TCC CAA GAC AGC TCC AGC ACC GCT	245
87	Leu Ala Trp Trp His Glu Trp Ala Ser Gln Asp Ser Ser Ser Thr Ala	
88	60 65 70	
90	TTC GAA GGG GGT ACC CCG GAG CTG TCT AAG CGG CAG GAA AGA CCA CCC	293
91	Phe Glu Gly Gly Thr Pro Glu Leu Ser Lys Arg Gln Glu Arg Pro Pro	
92	75 80 85	
94	CTC CAG CAG CCC CCA CAC CGG GAT AAA AAG CCC TGC AAG AAC TTC TTC	341
95	Leu Gln Gln Pro Pro His Arg Asp Lys Lys Pro Cys Lys Asn Phe Phe	
96	90 95 100	
98	TGG AAA ACC TTC TCC TCG TGC AAG TAGCCCGAGC CTGACCGGAG CCTGACCGGC	395
99	Trp Lys Thr Phe Ser Ser Cys Lys	
100	105 110	
102	CACCCTGTGA ATGCAGCCGT GGCCTGAATA AAGAGTGTCA AGT	438
105	(2) INFORMATION FOR SEQ ID NO: 2:	
107	(i) SEQUENCE CHARACTERISTICS:	
108	(A) LENGTH: 112 amino acids	
109	(B) TYPE: amino acid	
110	(D) TOPOLOGY: linear	
112	(ii) MOLECULE TYPE: protein	
113	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
115	Met Gly Gly Cys Ser Thr Arg Gly Lys Arg Pro Ser Ala Leu Ser Leu	
116	1 5 10 15	
118	Leu Leu Leu Leu Leu Leu Ser Gly Ile Ala Ala Ser Ala Leu Pro Leu	
119	20 25 30	
121	Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln Asp Ala Thr Gly Gly	
122	35 40 45	
124	Arg Arg Thr Gly Leu Leu Thr Phe Leu Ala Trp Trp His Glu Trp Ala	
125	50 55 60	
127	Ser Gln Asp Ser Ser Ser Thr Ala Phe Glu Gly Gly Thr Pro Glu Leu	
128	65 70 75 80	
130	Ser Lys Arg Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp	
131	85 90 95	

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133 Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
 134 100 105 110
 140 (2) INFORMATION FOR SEQ ID NO: 3:
 142 (i) SEQUENCE CHARACTERISTICS:
 143 (A) LENGTH: 110 amino acids
 144 (B) TYPE: amino acid
 145 (D) TOPOLOGY: linear
 147 (ii) MOLECULE TYPE: protein
 149 (v) FRAGMENT TYPE: C-terminal
 153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 155 Gln Cys Ala Leu Ala Ala Leu Cys Ile Val Leu Ala Leu Gly Gly Val
 156 1 5 10 15
 158 Thr Gly Ala Pro Ser Asp Pro Arg Leu Arg Gln Phe Leu Gln Lys Ser
 159 20 25 30
 161 Leu Ala Ala Ala Thr Gly Lys Gln Glu Leu Ala Lys Tyr Phe Leu Ala
 162 35 40 45
 164 Glu Leu Leu Ser Glu Pro Asn Gln Thr Glu Asn Asp Ala Leu Glu Pro
 165 50 55 60
 167 Glu Asp Leu Pro Gln Ala Ala Glu Gln Asp Glu Met Arg Leu Glu Leu
 168 65 70 75 80
 170 Gln Arg Ser Ala Asn Ser Asn Pro Ala Met Ala Pro Arg Glu Arg Lys
 171 85 90 95
 172 Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
 173 100 105 110
 175 (2) INFORMATION FOR SEQ ID NO: 4:
 177 (i) SEQUENCE CHARACTERISTICS:
 178 (A) LENGTH: 427 base pairs
 179 (B) TYPE: nucleic acid
 180 (C) STRANDEDNESS: single
 181 (D) TOPOLOGY: linear
 183 (ii) MOLECULE TYPE: cDNA
 185 (iii) HYPOTHETICAL: NO
 187 (iv) ANTI-SENSE: NO
 190 (ix) FEATURE:
 191 (A) NAME/KEY: CDS
 192 (B) LOCATION: 25..354
 195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 197 GCACGAGGCT CAGCACGTCC GAGG ATG ATG GGT GGC CGA GGC ACA GGA GGC 51
 198 Met Met Gly Gly Arg Gly Thr Gly Gly
 199 1 5
 201 AAG TGG CCC TCA GCC TTC GGG CTG CTG CTG CTC TGG GGG GTC GCA GCC 99
 202 Lys Trp Pro Ser Ala Phe Gly Leu Leu Leu Leu Trp Gly Val Ala Ala
 203 10 15 20 25
 205 TCC GCC CTT CCC CTG GAG AGT GGC CCT ACT GGC CAG GAC AGT GTG CAG 147
 206 Ser Ala Leu Pro Leu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
 207 30 35 40
 209 GAA GCC ACC GAG GGG AGG AGC GGC CTT CTG ACT TTC CTT GCC TGG TGG 195
 210 Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp
 211 45 50 55

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213 CAC GAG TGG GCT TCC CAA GCC AGC TCC AGC ACC CCC GTC GGA GGG GGT 243
 214 His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly
 215 60 65 70
 217 ACC CCC GGG CTG TCC AAG AGC CAG GAA AGG CCA CCC CCC CAA CAG CCC 291
 218 Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Pro Gln Gln Pro
 219 75 80 85
 221 CCA CAC CTG GAT AAA AAG CCC TGC AAG AAC TTC TTC TGG AAA ACC TTC 339
 222 Pro His Leu Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe
 223 90 95 100 105
 224 TCC TCG TGC AAG TAACCCACCT CTGGGCATAG CACCCTGGCC ACCCTGTGAG 391
 225 Ser Ser Cys Lys
 W--> 226 110
 228 ATGCCAACGA GACCTGAATA AAGACTGTCA ATCAAC 427
 231 (2) INFORMATION FOR SEQ ID NO: 5:
 233 (i) SEQUENCE CHARACTERISTICS:
 234 (A) LENGTH: 109 amino acids
 235 (B) TYPE: amino acid
 236 (D) TOPOLOGY: linear
 238 (ii) MOLECULE TYPE: protein
 240 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 242 Met Met Gly Gly Arg Gly Thr Gly Gly Lys Trp Pro Ser Ala Phe Gly
 243 1 5 10 15
 245 Leu Leu Leu Leu Trp Gly Val Ala Ala Ser Ala Leu Pro Leu Glu Ser
 246 20 25 30
 248 Gly Pro Thr Gly Gln Asp Ser Val Gln Glu Ala Thr Glu Gly Arg Ser
 249 35 40 45
 251 Gly Leu Leu Thr Phe Leu Ala Trp Trp His Glu Trp Ala Ser Gln Ala
 252 50 55 60
 254 Ser Ser Ser Thr Pro Val Gly Gly Gly Thr Pro Gly Leu Ser Lys Ser
 255 65 70 75 80
 257 Gln Glu Arg Pro Pro Pro Gln Gln Pro Pro His Leu Asp Lys Lys Pro
 258 85 90 95
 260 Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
 261 100 105
 264 (2) INFORMATION FOR SEQ ID NO: 6:
 266 (i) SEQUENCE CHARACTERISTICS:
 267 (A) LENGTH: 85 amino acids
 268 (B) TYPE: amino acid
 269 (D) TOPOLOGY: linear
 271 (ii) MOLECULE TYPE: protein
 273 (v) FRAGMENT TYPE: C-terminal
 277 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 279 Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
 280 1 5 10 15
 281 Asp Ala Thr Gly Gly Arg Arg Thr Gly Leu Leu Thr Phe Leu Ala Trp
 282 20 25 30
 284 Trp His Glu Trp Ala Ser Gln Asp Ser Ser Ser Thr Ala Phe Glu Gly
 285 35 40 45
 287 Gly Thr Pro Glu Leu Ser Lys Arg Gln Glu Arg Pro Pro Leu Gln Gln

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Output Set: N:\CRF3\03262002\J062375.raw

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288          50          55          60
290    Pro Pro His Arg Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr
291      65          70          75          80
293    Phe Ser Ser Cys Lys
294          85
296 (2) INFORMATION FOR SEQ ID NO: 7:
298   (i) SEQUENCE CHARACTERISTICS:
299       (A) LENGTH: 29 amino acids
300       (B) TYPE: amino acid
301       (D) TOPOLOGY: linear
303   (ii) MOLECULE TYPE: protein
305   (v) FRAGMENT TYPE: C-terminal
309   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
311    Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp Lys Lys Pro
312      1          5          10          15
314    Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
315          20          25
317 (2) INFORMATION FOR SEQ ID NO: 8:
319   (i) SEQUENCE CHARACTERISTICS:
320       (A) LENGTH: 14 amino acids
321       (B) TYPE: amino acid
322       (D) TOPOLOGY: linear
324   (ii) MOLECULE TYPE: protein
326   (v) FRAGMENT TYPE: C-terminal
330   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
332    Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
333      1          5          10
335 (2) INFORMATION FOR SEQ ID NO: 9:
337   (i) SEQUENCE CHARACTERISTICS:
338       (A) LENGTH: 13 amino acids
339       (B) TYPE: amino acid
340       (D) TOPOLOGY: linear
342   (ii) MOLECULE TYPE: protein
344   (v) FRAGMENT TYPE: internal
348   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
350    Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp
351      1          5          10
353 (2) INFORMATION FOR SEQ ID NO: 10:
355   (i) SEQUENCE CHARACTERISTICS:
356       (A) LENGTH: 84 amino acids
357       (B) TYPE: amino acid
358       (D) TOPOLOGY: linear
360   (ii) MOLECULE TYPE: protein
362   (v) FRAGMENT TYPE: C-terminal
366   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
368    Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
369      1          5          10          15
371    Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp
372          20          25          30

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/062,375

DATE: 03/26/2002

TIME: 09:30:32

Input Set : N:\Cr3\RULE60\10062375.raw

Output Set: N:\CRF3\03262002\J062375.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4